

<http://dx.doi.org/10.35630/2199-885X/2020/10/4.18>

EVALUATION OF THE ORAL MICROBIOTA IN ENT AND DENTAL PATIENTS

Received 17 September 2020;
Received in revised form 15 October 2020;
Accepted 19 October 2020

Vladimir Dumanov¹ , Nadezda Novikova² ,
Artem Morozov² , Anastasia Morozova ,
Sergey Zhukov, Anastasiia Pichugova 

¹ The Moscow Research and Clinical Center for Tuberculosis Control, Moscow

² Tver State Medical University, Tver

✉ ammorozovv@gmail.com

ABSTRACT — The World Health Organisation estimates oropharyngeal mycosis as the second most common fungal infections (40% of all cases). The study of microbiocenoses and their role in maintaining health and the development of pathology is a complex multifactorial problem which includes the study of not only the microbial communities themselves but also the components and metabolites of microflora as well as their interaction with a macroorganism considering personification and social factors. Our study was aimed to evaluate possible microbial scenery changes using microscopic examination of pharynx and oral cavity specimens from patients at departments of otolaryngology and dentistry of Polyclinic No. 1 (Tver, Russia). The investigation of samples of dorsal surface of patients' tongues (503 participants) was carried out between January 2018 and October 2020. The selection criterion met the patients with the following symptoms: swallowing difficulties, feeling of a “lump in the throat”, a sore throat, a dry mouth, a burning tongue. Our findings showed the persistence of fungal infection of the oral cavity in 68,5% of cases with numerous otolaryngological and dental diseases. *Candida albicans* microbial associations with cocci as well as combinations with mixed microflora were identified in 45% of cases. Anatomical and functional aspects of the oral cavity account for an interdisciplinary approach to the treatment of such patients with a close cooperation between otolaryngologists and dentists.

KEYWORDS — microbial scenery, pathogenic microflora, oropharynx, oral cavity, mucosa.

INTRODUCTION

According to the data, provided by the World Health Organisation, one fifth of the world's population suffers from various fungal infections, the second most common of which (40% of all cases) is oropharyngeal mycosis. Its main causative agent (*Candida albicans*) is an opportunistic microorganism that is a part of the normal microflora of the mucosa of the gastrointestinal and urogenital tract. Oropharyngeal

mycosis is accompanied by a burning and dry tongue, a bad taste in the mouth and discomfort while swallowing. Oral cavity, which determines the state of human health, constitutes a comprehensive, unique microecological system, closely linked both to the internal environment of an organism as well as to the external one [1, 2].

The study of microbiocenoses and their role in maintaining health and the development of pathology is a complex multifactorial problem which includes the study of not only the microbial communities but also the components and metabolites of microflora as well as their interaction with a macroorganism considering personification and social factors. It is known that in terms of quantitative and qualitative diversity, the oral mucosa is a fairly extensive biotope, and bacteria demonstrate specific tropism in relation to various anatomical oral cavity surfaces. Teeth, gums, gingival fluid, gingival grooves, the mucosa of the tongue, cheeks, hard and soft palates, ducts of salivary glands with their saliva have significant differences in the microbial communities composition, as well as the existence of a separate tonsillar microbiome [3]. The oral cavity microbiota determines colonisation resistance, local immune resistance and the microecosystems formation not only of its own biotope, but also of the entire gastrointestinal tract, the biotope of the broncho-pulmonary system [4].

The purpose of the study was to evaluate possible changes of microbial scenery using microscopic examination of pharynx and oral cavity samples from ENT and dental patients.

MATERIAL AND METHODS

The evaluation of clinical specimens taken from the dorsal surface of patients' tongues (503 participants) was carried out directly in Polyclinic No. 1 of Tver State Clinical Hospital No. 7 (Russia), between January 2018 and October 2020. Patients for participation at the research were selected by the following complaints: swallowing difficulties, a feeling of a “lump in the throat”, a sore throat, a dry mouth, a burning tongue. 503 patients took part in the investigation: 18,84% of them were male and 81,16% were female, both in the age between 18 and 80 years old. The clinical material from the tongue surface was captured on the slide with a sterile cotton, followed by Gram-staining and a microscopic research. The findings were

systematized and processed with the licensed software Microsoft Excel 2016.

RESULTS AND DISCUSSION

As a result of the microscopic examination of oral cavity and pharynx samples in 503 patients mycotic mycelium filaments and fungal bodies were detected in various amounts in 68,59% (345 patients). A negative result of detecting mycotic filaments and mycelium was observed in 31,41% (158 patients). Variations in the number of fungal bodies also occurred in their combination with bacteria (45,72%), among which associations of fungi and representatives of the cocco-diplococcal flora accounted for 20,48% (103 cases), and the combination of fungi and representatives of mixed flora were found in 22,267% (112 cases). It should be noted that a combination of an insignificant amount of coccal flora and single elements of the fungus were found in 2,98% (15 cases). Fungal mycelium filaments, both single and in the form of myco-bacterial associations were identified in 14,71% (74 cases). Individual elements of the fungus and their associations were detected in 2,98% (15 cases), elements of the fungus and their associations — in 25,65% (129 cases), elements of the fungus + and their associations — in 16,30% (82 cases), elements of the fungus +++ and their associations — in 8,95% (45 cases), Table 1.

The outcomes of our research, in 68,5% of all cases of various otolaryngological and dental diseases revealed the persistence of fungal infection of the oral cavity. In 45% there were *Candida albicans* microbial associations with cocci (the genus *Streptococcus*, the genus *Staphylococcus*) as well as combinations with mixed microflora (representatives of the families *Pseudomonadaceae* and *Enterobacteriaceae*, the genus *Corynebacterium*, the genus *Clostridium*, the genus *Lactobacillus*, the genus *Rothia*, the genus *Actinomyces*). It should be noted that the identified microorganisms in conjunction with the anamnesis data, complaints and objective examination may indicate various types and degrees of oral cavity and oropharynx microbiome disorder. The obtained data correspond to the data of literature sources on the presence of the phenomena of oral cavity and oropharynx microbiome symbiosis and commensalism.

According to the literature, 99% of bacteria exist in the form of biofilms attached to the substrate, and they are more resistant to the immune system factors and antibiotics. The reason for this phenomenon is simple - bacteria included into the substrate in the form of biofilms acquire qualitatively new properties [5]. An interesting fact is that synergistic interactions between fungi of the genus *Candida albicans* and commensal streptococci exert an important role in

Table 1. Microbial scenery variation of the investigated material

The results of microscopic research	%	Absolute quantity
Mycelium of the fungus was not revealed	20,67	104
Fungus mycelium filaments	3,38	17
Funguselements +	11,94	60
Fungus elements ++	4,57	23
Fungus elements +++	2,98	15
Insignificant coccal flora, isolated elements of the fungus	2,98	15
Moderate coccal flora, fungus elements were not detected	2,18	11
Abundant coccal flora, fungus elements were not detected	4,37	22
Abundant coccal-diplococcal flora, fungus elements +	11,54	58
Abundant coccal-diplococcal flora, fungus elements ++	6,36	32
Abundant coccal-diplococcal flora, fungus elements +++	2,58	13
Abundant mixed flora, fungus elements were not detected	4,17	21
Abundant mixed flora, fungal mycelium	11,34	57
Abundant mixed flora, fungal elements +	2,19	11
Abundant mixed flora, fungal elements ++	5,37	27
Abundant mixed flora, fungal elements +++	3,38	17
Total number of carried out studies	100	503

the transition of the relationship from commensalism to pathogenetic impact on oral mucosa, causing deep damage. At the same time it is important to emphasize the fact that in this case streptococci grow in close contact with the oral mucosa while fungi grow on the bacterial surface [6]. Researchers distinguish resident (permanent), additional (transient) and random microflora. On the oral mucosa among bacterial spectrum prevail microorganisms belonging to the genus *Streptococcus* (*S. viridans*, *S. pyogenes*, *S. pneumoniae*, *S. oralis*), the genus *Staphylococcus* (*S. aureus*, *S. epidermidis*, *S. hominis*), *Corynebacterium* (*C. tuberculo-stearicum*, *C. pseudodiphtheriticum*, *C. aurimucosum*, *C. amycolatum*, *C. durum*, *C. afermentasilipophilum*, *C. minutissimum*, *C. urealyticum*, *C. propinquum*), *Candida albicans* and *Actinomyces viscosus* are identified in a single quantity [1, 2, 3]. In the structure of palatine tonsils microbial scenery α - and γ -hemolytic streptococci (*S. parasanguinis*, *S. mitis*, *S. salivarius*, *S. Oligofermentans*), gram-positive bacteria of the genus *Rothia* (*R. mucilaginosa*, *R. dentocariosa*) dominates. Among the microorganisms of the genus *Actinomyces spp. oral* and the genus *Staphylococcus aureus*. There are also bacteria belonging to the genus *Corynebacterium* (*C. accolens*, *C. tuberculo-stearicum*) in the biotope of tonsils.

With a change in the quantity and quality of the resident microflora composition, oral functional fullness and anatomic integrity disorders, the residents of the transient microflora actively form etiopathogenetic links in the occurrence of pathologic processes leading to the oral mucosa dysbiosis. This means that the oral microflora, as a highly sensitive indicator, reacts with qualitative and quantitative shifts to changes in the state of organs and systems of the human body as a whole.

CONCLUSIONS

Fungal flora is prevailing in oral cavity area of ENT and dental patients, which have to be subjected to a specific antifungal therapy to stimulate the growth of oral and oropharynx microflora. Due to anatomical and functional aspects of the oral cavity and pharynx, the search of treatment solutions for such patients requires an interdisciplinary approach and a close cooperation between otolaryngologists and dentists.

Author Contributions

Authors contributed to the manuscript equally.

REFERENCES

1. **ARWEILER N, NETUSCHIL L.** The oral microbiota. *Advances in Experimental Medicine and Biology*. 2016;902:45–60. <https://doi.org/10.1007/978-3-319-31248-4>
2. **WILLIAM H. BOWEN, ROBERT A. BURNE, HUI WU, HYUN KOO,** Oral Biofilms: Pathogens, Matrix, and Polymicrobial Interactions in Microenvironments. *Trends in Microbiology*, Volume 26, Issue 3, 2018, Pages 229–242, ISSN 0966-842X, <https://doi.org/10.1016/j.tim.2017.09.008>.
3. **TAKAHASHI N.** Oral Microbiome Metabolism: From "Who Are They?" to "What Are They Doing?" // *Journal of Dental Research*. – 2015. – V. 94 (12). – P. 1628–1637.
4. **LAMONT RJ, KOO H, HAJISHENGALLIS G.** The oral microbiota: dynamic communities and host interactions. *Nat Rev Microbiol*. 2018 Dec;16(12):745–759. doi: 10.1038/s41579-018-0089-x. PMID: 30301974; PMCID: PMC6278837.
5. **LAMONT RJ, HAJISHENGALLIS G.** Polymicrobial synergy and dysbiosis in inflammatory disease. *Trends Mol Med*. 2015 Mar;21(3):172–83. doi: 10.1016/j.molmed.2014.11.004. Epub 2014 Nov 20. PMID: 25498392; PMCID: PMC4352384.
6. **BERTOLINI M.M., XU H., SOBUE T., NOBILE C.J., DEL BELCURY A.A.** Candida-streptococcal mucosal biofilms display distinct structural and virulence characteristics depending on growth conditions and hyphal morphotypes. *Mol. Oral Microbiol*. 2015; 30 (4): 307–22. Epub 2015 Apr 20. DOI: 10.1111/omi.12095.